

SCORE Search Results Details for Application 10521049 and Search Result 20071113_120427_us-10-521-049-12.rng.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2007, 12:10:03 ; Search time 1016 Seconds
(without alignments)
4595.135 Million cell updates/sec

Title: US-10-521-049-12
Perfect score: 630
Sequence: 1 atcgccacaccgcggggagc.....agacagaccacggggcgag 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|----------|--------------------|
| 1 | 630 | 100.0 | 630 | 12 | ADI81791 | Adi81791 Human tau |
| 2 | 630 | 100.0 | 702 | 12 | ADI81790 | Adi81790 Human tau |
| 3 | 630 | 100.0 | 720 | 12 | ADI81793 | Adi81793 Human tau |
| 4 | 630 | 100.0 | 792 | 12 | ADI81792 | Adi81792 Human tau |
| 5 | 630 | 100.0 | 876 | 12 | ADI81789 | Adi81789 Human tau |
| 6 | 630 | 100.0 | 1059 | 2 | AAT69790 | Aat69790 Human tau |
| 7 | 630 | 100.0 | 1059 | 2 | AAX75754 | Aax75754 Human mic |
| 8 | 630 | 100.0 | 1107 | 3 | AAZ29262 | Aaz29262 Human Tau |
| 9 | 630 | 100.0 | 1108 | 6 | ABK83763 | Abk83763 Human cDN |
| 10 | 630 | 100.0 | 1108 | 15 | AEE60794 | Aee60794 Human pat |
| 11 | 630 | 100.0 | 1108 | 15 | AEF92680 | Aef92680 Human Tau |
| 12 | 630 | 100.0 | 1108 | 15 | AEG70585 | Aeg70585 Human p53 |
| 13 | 630 | 100.0 | 1233 | 15 | AEL56834 | Ael56834 Human mic |
| 14 | 630 | 100.0 | 2174 | 15 | AEL56822 | Ael56822 Human mic |
| 15 | 630 | 100.0 | 2308 | 15 | AEL56824 | Ael56824 Human mic |
| 16 | 630 | 100.0 | 2529 | 6 | ABQ80742 | Abq80742 Human Tau |
| 17 | 630 | 100.0 | 2529 | 14 | ADV42372 | Adv42372 Human Tau |
| 18 | 630 | 100.0 | 2529 | 14 | ADU82408 | Adu82408 Human Tau |
| 19 | 630 | 100.0 | 2529 | 14 | ADV86197 | Adv86197 Human bra |
| 20 | 630 | 100.0 | 2529 | 14 | ADV51196 | Adv51196 Human Tau |
| 21 | 630 | 100.0 | 2529 | 14 | ADZ88275 | Adz88275 Human tau |
| 22 | 630 | 100.0 | 2529 | 14 | ADZ85405 | Adz85405 Human Tau |
| 23 | 630 | 100.0 | 2529 | 14 | AEA37348 | Aea37348 Human Tau |
| 24 | 630 | 100.0 | 2529 | 14 | AEA37361 | Aea37361 Human Tau |
| 25 | 630 | 100.0 | 2529 | 14 | AEA37374 | Aea37374 Human Tau |
| 26 | 630 | 100.0 | 2529 | 14 | AEA37387 | Aea37387 Human Tau |
| 27 | 626.8 | 99.5 | 1107 | 1 | AAN91707 | Aan91707 Paired he |

SCORE Search Results Details for Application 10521049 and Search Result 20071113_120428_us-10-521-049-12.rge.

| | | | | |
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OM nucleic - nucleic search, using sw model

Run on: November 13, 2007, 12:04:43 ; Search time 10186 Seconds
(without alignments)
4275.063 Million cell updates/sec

Title: US-10-521-049-12
Perfect score: 630
Sequence: 1 atcgccacaccgcggggagc.....agacagaccacggggcgag 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|----------|--------------------|
| 1 | 630 | 100.0 | 630 | 2 | CQ768352 | CQ768352 Sequence |
| 2 | 630 | 100.0 | 630 | 2 | DD261347 | DD261347 Transgeni |
| 3 | 630 | 100.0 | 702 | 2 | CQ768351 | CQ768351 Sequence |
| 4 | 630 | 100.0 | 702 | 2 | DD261346 | DD261346 Transgeni |
| 5 | 630 | 100.0 | 720 | 2 | CQ768354 | CQ768354 Sequence |
| 6 | 630 | 100.0 | 720 | 2 | DD261349 | DD261349 Transgeni |
| 7 | 630 | 100.0 | 792 | 2 | CQ768353 | CQ768353 Sequence |
| 8 | 630 | 100.0 | 792 | 2 | DD261348 | DD261348 Transgeni |
| 9 | 630 | 100.0 | 876 | 2 | CQ768350 | CQ768350 Sequence |
| 10 | 630 | 100.0 | 876 | 2 | DD261345 | DD261345 Transgeni |
| 11 | 630 | 100.0 | 1059 | 2 | A62328 | A62328 Sequence 16 |
| 12 | 630 | 100.0 | 1059 | 2 | A62330 | A62330 Sequence 18 |
| 13 | 630 | 100.0 | 1059 | 2 | A62332 | A62332 Sequence 20 |
| 14 | 630 | 100.0 | 1059 | 2 | AR075561 | AR075561 Sequence |
| 15 | 630 | 100.0 | 1059 | 2 | BD084809 | BD084809 Diagnosis |
| 16 | 630 | 100.0 | 1059 | 5 | BT006772 | BT006772 Homo sapi |
| 17 | 630 | 100.0 | 1059 | 8 | AY889347 | AY889347 Synthetic |
| 18 | 630 | 100.0 | 1059 | 8 | AY889348 | AY889348 Synthetic |
| 19 | 630 | 100.0 | 1059 | 8 | AY891838 | AY891838 Synthetic |
| 20 | 630 | 100.0 | 1059 | 8 | BT007911 | BT007911 Synthetic |
| 21 | 630 | 100.0 | 1107 | 2 | I17644 | I17644 Sequence 1 |
| 22 | 630 | 100.0 | 1108 | 2 | A08372 | A08372 Synthetic n |
| 23 | 630 | 100.0 | 1108 | 2 | CS239175 | CS239175 Sequence |
| 24 | 630 | 100.0 | 1108 | 5 | HUMTAUA | J03778 Human micro |
| 25 | 630 | 100.0 | 1173 | 2 | AR030346 | AR030346 Sequence |
| 26 | 630 | 100.0 | 1173 | 2 | AR062941 | AR062941 Sequence |
| 27 | 630 | 100.0 | 1391 | 5 | BC000558 | BC000558 Homo sapi |
| 28 | 630 | 100.0 | 2252 | 5 | BC099721 | BC099721 Homo sapi |
| 29 | 630 | 100.0 | 2252 | 5 | BC101936 | BC101936 Homo sapi |
| 30 | 630 | 100.0 | 2253 | 5 | BC098281 | BC098281 Homo sapi |
| 31 | 630 | 100.0 | 2254 | 5 | BC114504 | BC114504 Homo sapi |
| 32 | 630 | 100.0 | 2527 | 2 | CQ723152 | CQ723152 Sequence |
| 33 | 630 | 100.0 | 2529 | 2 | AX522066 | AX522066 Sequence |
| 34 | 630 | 100.0 | 6794 | 5 | AK226139 | AK226139 Homo sapi |
| 35 | 628.4 | 99.7 | 1173 | 2 | AR152002 | AR152002 Sequence |
| 36 | 625.2 | 99.2 | 732 | 5 | AY526356 | AY526356 Homo sapi |
| 37 | 609.8 | 96.8 | 748 | 5 | AY369830 | AY369830 Pan trogl |
| 38 | 592.2 | 94.0 | 3122 | 5 | AK095802 | AK095802 Homo sapi |
| 39 | 579.4 | 92.0 | 1059 | 5 | S83356 | S83356 {pseudogene |
| 40 | 527 | 83.7 | 723 | 2 | CQ768343 | CQ768343 Sequence |
| 41 | 527 | 83.7 | 723 | 2 | DD261338 | DD261338 Transgeni |
| 42 | 527 | 83.7 | 795 | 2 | CQ768342 | CQ768342 Sequence |
| 43 | 527 | 83.7 | 795 | 2 | DD261337 | DD261337 Transgeni |
| 44 | 527 | 83.7 | 813 | 2 | CQ768345 | CQ768345 Sequence |
| 45 | 527 | 83.7 | 813 | 2 | DD261340 | DD261340 Transgeni |